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**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

*-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --*

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE <u>03</u> MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.
- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

1)☒ Responsive to communication(s) filed on <u>14 September 2009</u>.
2a)☐ This action is **FINAL**.  2b)☒ This action is non-final.
3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

4)☒ Claim(s) <u>85-110 and 112</u> is/are pending in the application.

    4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.
6)☒ Claim(s) <u>85-110 and 112</u> is/are rejected.
7)☐ Claim(s) _____ is/are objected to.
8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

**Application Papers**

9)☐ The specification is objected to by the Examiner.
10)☒ The drawing(s) filed on <u>21 April 2005</u> is/are: a)☒ accepted or b)☐ objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

    Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

    a)☐ All  b)☐ Some * c)☐ None of:

      1.☐ Certified copies of the priority documents have been received.

      2.☐ Certified copies of the priority documents have been received in Application No. _____.

      3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

    * See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

1)☒ Notice of References Cited (PTO-892)
2)☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3)☐ Information Disclosure Statement(s) (PTO/SB/08)
    Paper No(s)/Mail Date _____.

4)☐ Interview Summary (PTO-413)
    Paper No(s)/Mail Date. _____.
5)☐ Notice of Informal Patent Application
6)☐ Other: _____.

## DETAILED ACTION

### *Continued Examination Under 37 CFR 1.114*

1.       A request for continued examination under 37 CFR 1.114, including the

fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection.

Since this application is eligible for continued examination under 37 CFR 1.114,

and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the

previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's

submission filed on September 14, 2009 has been entered.

### *Response to Amendment*

2.       **Claim 111** is canceled.

**Claims 85-110**, and **112** are pending.

### *Response to Arguments*

3.       Objection to the **claim 110** is withdrawn.

4.       The 35 U.S.C. 112, second paragraph, rejections of **claims 94-102** are

withdrawn in view of Applicant's amendment.

5.       The 35 U.S.C. 101 rejections of **claims 103-110**, and **112** are withdrawn

in view of Applicant's amendment.

6.       Applicant's arguments with respect to the 35 U.S.C. 103(a) rejections of

the pending claims have been considered but are moot in view of the new

grounds of rejection presented hereon.

## *Claim Rejections - 35 USC § 103*

7.    The following is a quotation of 35 U.S.C. 103(a) which forms the basis for

all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described
> as set forth in section 102 of this title, if the differences between the subject matter sought to
> be patented and the prior art are such that the subject matter as a whole would have been
> obvious at the time the invention was made to a person having ordinary skill in the art to which
> said subject matter pertains.  Patentability shall not be negatived by the manner in which the
> invention was made.

8.    **Claims 85-93** are rejected under 35 U.S.C. 103(a) as being unpatentable

by <u>Wallace et al.</u> (*Pat. No. US 6,920,396, filed on September 20, 2001;*

*hereinafter <u>Wallace</u>*) in view of <u>Algate et al.</u> (*Pub. No. US 2003/0118599, filed on*

*May 10, 2002; hereinafter <u>Algate</u>*).

Regarding **claim 85**, <u>Wallace</u> clearly shows and discloses a method for

managing a biological database (*Abstract*), comprising:

a. receiving a set of biological sequences (*A set of search query*

*parameters specifying a plurality of sequence sets are received*, [Column 3,

Lines 12-14]);

b. querying a plurality of databases with the set of biological sequences

(*The structured database query is executed in a database layer. At least one*

*queue handler loading the structured database query is provided. A plurality of*

*biological data repositories are selected*, [Column 3, Lines 32-34]);

c. receiving query results from the plurality of databases (*Search query*

*parameters are accepted for and search* results displayed from a search request

for multiple sequence sets *performed against a plurality of biological data*

*repositories in a user interface layer,* [Column 3, Lines 24-28]);

    d. storing the query results in a biological database (*The relational*

*database 33 stores tables and queues relating to search requests and results as*

*transacted by the Blast Node 18,* [Column 4, Lines 65-67]), wherein each

sequence in the set of biological sequences is associated with a respective

record comprising query results from each of the plurality of databases (*Each*

*biological data repository contains sequence data stored into unstructured*

*records which are each identified by a unique identifier. The structured database*

*query is executed against at least one database engine. The database results*

*are obtained from the selected biological data repositories,* [Column 3, Lines 35-

40]);

    e. periodically performing steps b-d (*During each iteration (block 232), the*

*Blast node 53 searches the search queue 43 (shown in FIG. 2) for those entries*

*having a status equal to zero (block 233). A status of zero indicates that no*

*search results are present. If no entries are found (block 234), the Blast node 53*

*sleeps for a pre-determined interval (block 235). In the described embodiment,*

*an interval of 2,000 milliseconds is used, although other suitable intervals could*

*also be used,* [Column 11, Lines 4-12]);

    f. receiving, from a user, a request to view a record of one of the set of

biological sequences; and g. displaying an executive summary of the record of

one of the set of biological sequences (*FIG. 6 is a screenshot 100 showing, by*

*way of example, a Web page for displaying a search summary. The search*

*summary is presented as a table 101 listing out in columns the search name 102,*

*requested user 103, date 104, sequence set 105, databases 106, and deletion*

*flag 107. The table 101 is necessary to display the individual results based on the*

*specified database and requesting sequence, as each search can include*

*multiple sequences and multiple databases. Individual search results can be*

*deleted by pressing the "Delete Searches" button 108. Detailed search results*

*can be obtained by selecting an appropriate search name 102*, [Column 8, Lines

35-45]).

Algate discloses the results comprise at least comprise at least

immunohistological data, *in situ* hybridization data, functional data, expression

data, and structural data ([0723] and [0809]).

It would have been obvious to an ordinary person skilled in the art at the

time of the invention was made to incorporate the teachings of Algate with the

teachings of Wallace for the purpose of utilizing polypeptides and polynucleotides

to produce pharmaceutical compositions, e.g., vaccines, and other compositions

for the diagnosis and treatment of lung cancer ([0002] of Algate).

Regarding **claim 86**, Wallace further discloses the set of biological

sequences comprises one or more of, nucleic acid sequences and amino acid

sequences (*Figure 4 shows for a new biological data search request, the user*

*enters a search description 71 in a search description text box 72, followed by*

*either a new set of FASTA formatted sequences 73 in a formatted sequence set*

*text box 74, a local file 75 in a local file text box 76, or an existing sequence set*

*77 in an existing sequence set text box 78*, [Column 7, Line 63 → Column 8, Line

2]).

Regarding **claim 87**, <u>Wallace</u> further discloses receiving the set of

biological sequences comprises receiving the set of biological sequences from a

user (*Figure 4 shows for a new biological data search request, the user enters a*

*search description 71 in a search description text box 72, followed by either a*

*new set of FASTA formatted sequences 73 in a formatted sequence set text box*

*74, a local file 75 in a local file text box 76, or an existing sequence set 77 in an*

*existing sequence set text box 78*, [Column 7, Line 63 → Column 8, Line 2]).

Regarding **claim 88**, <u>Algate</u> further discloses the query results further

comprise complementary deoxyribonucleic acid (eDNA) data, expressed

sequence tags, and pharmacology data (*Initial characterization of the cDNA*

*expression library was performed by randomly sequencing 24 primary*

*transformants and subjecting the resulting sequences to BLAST searches*

*against available databases. The determined cDNA sequences are provided in*

*SEQ ID NO: 443-480, with the results of the BLAST searches being provided in*

*Table 4*, [0998]), expressed sequence tags (*Comparison of the isolated*

*sequences with those in the public database revealed no significant homologies*

*to the sequences of SEQ ID NO: 151, 153 and 154. The sequences of SEQ ID*

*NO: 149, 152, 156, 157 and 158 were found to show some homology to*

*previously isolated expressed sequence tags (ESTs), [0973]).*

Regarding **claim 89**, Wallace further discloses the plurality of databases

comprises two or more of National Center for Biotechnology Information (NCBI)

databases or other externally curated and maintained specialized databases

(*Figure 6*).

Regarding **claim 90**, Wallace further discloses periodically performing

steps b-d comprises performing steps b-d daily (*During each iteration (block*

*232), the Blast node 53 searches the search queue 43 (shown in FIG. 2) for*

*those entries having a status equal to zero (block 233). A status of zero indicates*

*that no search results are present. If no entries are found (block 234), the Blast*

*node 53 sleeps for a pre-determined interval (block 235). In the described*

*embodiment, an interval of 2,000 milliseconds is used, although other suitable*

*intervals could also be used*, [Column 11, Lines 4-12]).

Regarding **claim 91**, Wallace further discloses performing one or more

bioinformatics functions on the set of biological sequences or the query results

(*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for*

*displaying a search summary. The search summary is presented as a table 101*

*listing out in columns the search name 102, requested user 103, date 104,*

*sequence set 105, databases 106, and deletion flag 107. The table 101 is*

*necessary to display the individual results based on the specified database and*

*requesting sequence, as each search can include multiple sequences and*

*multiple databases. Individual search results can be deleted by pressing the*

*"Delete Searches" button 108. Detailed search results can be obtained by*

*selecting an appropriate search name 102,* [Column 8, Lines 35-45]).

Regarding **claim 92**, <u>Wallace</u> further discloses the one or more

bioinformatics functions comprises one or more of sequence alignment, gene

identification, protein identification structure prediction, motif comparison, and

biological text analysis (*FIG. 6 is a screenshot 100 showing, by way of example,*

*a Web page for displaying a search summary. The search summary is presented*

*as a table 101 listing out in columns the search name 102, requested user 103,*

*date 104, sequence set 105, databases 106, and deletion flag 107. The table 101*

*is necessary to display the individual results based on the specified database*

*and requesting sequence, as each search can include multiple sequences and*

*multiple databases. Individual search results can be deleted by pressing the*

*"Delete Searches" button 108. Detailed search results can be obtained by*

*selecting an appropriate search name 102,* [Column 8, Lines 35-45]).

Regarding **claim 93**, <u>Wallace</u> further discloses displaying an executive

summary of the record of one of the set of biological sequences comprises

formatting the requested record for output to the user (*FIG. 6 is a screenshot 100*

*showing, by way of example, a Web page for displaying a search summary. The*

*search summary is presented as a table 101 listing out in columns the search*

*name 102, requested user 103, date 104, sequence set 105, databases 106, and*

*deletion flag 107. The table 101 is necessary to display the individual results*

*based on the specified database and requesting sequence, as each search can*

*include multiple sequences and multiple databases. Individual search results can*

*be deleted by pressing the "Delete Searches" button 108. Detailed search results*

*can be obtained by selecting an appropriate search name 102*, [Column 8, Lines

35-45]).

9.     **Claims 94-110**, and **112** are rejected under 35 U.S.C. 103(a) as being

unpatentable by <u>Wallace et al.</u> (*Pat. No. US 6,920,396, filed on September 20,*

*2001; hereinafter <u>Wallace</u>*) in view of <u>Algate et al.</u> (*Pub. No. US 2003/0118599,*

*filed on May 10, 2002; hereinafter <u>Algate</u>*), and further in view of <u>Gibson et al.</u>

(*Pub. No. US 2003/0055683, filed on September 19, 2002; hereinafter <u>Gibson</u>*).

Regarding **claim 94**, <u>Wallace</u> clearly shows and discloses a method

(*Abstract*) for managing a biological database, comprising:

f. receiving a set of biological sequences (*A set of search query*

*parameters specifying a plurality of sequence sets are received*, [Column 3,

Lines 12-14]);

g. querying a plurality of databases with the set of biological sequences

(*The structured database query is executed in a database layer. At least one*

*queue handler loading the structured database query is provided. A plurality of*

*biological data repositories are selected*, [Column 3, Lines 32-34]);

h. receiving query results from the plurality of databases (*Search query*

*parameters are accepted for and search* results displayed from a search request

for multiple sequence sets *performed against a plurality of biological data*

*repositories in a user interface layer*, [Column 3, Lines 24-28]);

i. storing the query results in a biological database (*The relational*

*database 33 stores tables and queues relating to search requests and results as*

*transacted by the Blast Node 18*, [Column 4, Lines 65-67]), wherein each

sequence in the set of biological sequences is associated with a respective

record comprising query results from each of the plurality of databases (*Each*

*biological data repository contains sequence data stored into unstructured*

*records which are each identified by a unique identifier. The structured database*

*query is executed against at least one database engine. The database results*

*are obtained from the selected biological data repositories*, [Column 3, Lines 35-

40]);

j. receiving, from a user, a request to view a record of one of the set of

biological sequences; and k. displaying an executive summary of the record of

one of the set of biological sequences (*FIG. 6 is a screenshot 100 showing, by*

*way of example, a Web page for displaying a search summary. The search*

*summary is presented as a table 101 listing out in columns the search name 102,*

*requested user 103, date 104, sequence set 105, databases 106, and deletion*

*flag 107. The table 101 is necessary to display the individual results based on the specified database and requesting sequence, as each search can include multiple sequences and multiple databases. Individual search results can be deleted by pressing the "Delete Searches" button 108. Detailed search results can be obtained by selecting an appropriate search name 102*, [Column 8, Lines 35-45]).

Algate discloses the results comprise at least comprise at least immunohistological data, *in situ* hybridization data, functional data, expression data, and structural data ([0723] and [0809]).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Algate with the teachings of Wallace for the purpose of utilizing polypeptides and polynucleotides to produce pharmaceutical compositions, e.g., vaccines, and other compositions for the diagnosis and treatment of lung cancer ([0002] of Algate).

Gibson discloses:

a. providing a plurality of databases (*The PRID system 10 includes client systems 16a, 16b, and 16c. Each client has applications and a local database 17a, 17b, and 17c*, [0024]);

b. determining the version of each of the plurality of databases (*At step 82, the server update process 80 then accesses the appropriate databases to determine if there are updates to the predetermined list of databases. The predetermined list of databases includes, but is not limited to, the FDA,*

*prescription drug databases, MSDS, or, O/S operating system databases or the like*, [0047]);

c. determining if the version of each of the plurality of databases is a current version (*After accessing the predetermined databases, the server update process then determines if there is new data or updates to existing data at step 83*, [0047]);

d. downloading the current version of any of the plurality of databases that is not a current version (*the clients systems 16(a-c) connect to the server 11, the modification files associated with the client are transmitted to the client to be used for updating each client's individual database*, [0025]);

e. periodically performing b-d (*Periodically, an update file is created for each client with all relevant changes since the last modification of the client database. When the clients systems 16(a-c) connect to the server 11, the modification files associated with the client are transmitted to the client to be used for updating each client's individual database*, [0025]).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of <u>Gibson</u> with the teachings of <u>Wallace</u>, as modified by <u>Algate</u>, for the purpose of creating update drug data for addition to the original drug information, and a transmit mechanism that transmits the update drug data to the remote device upon receiving a request from a remote device for the update drug data ([Abstract] of <u>Gibson</u>).

Regarding **claim 95**, <u>Wallace</u> further discloses the plurality of databases

comprises two or more of, National Center for Biotechnology Information (NCBI)

databases or other externally curated and maintained specialized databases

(*Figure 6*).

Regarding **claim 96**, <u>Wallace</u> further discloses periodically performing

steps b-d comprises performing steps b-d daily (*During each iteration (block*

*232), the Blast node 53 searches the search queue 43 (shown in FIG. 2) for*

*those entries having a status equal to zero (block 233). A status of zero indicates*

*that no search results are present. If no entries are found (block 234), the Blast*

*node 53 sleeps for a pre-determined interval (block 235). In the described*

*embodiment, an interval of 2,000 milliseconds is used, although other suitable*

*intervals could also be used*, [Column 11, Lines 4-12]).

Regarding **claim 97**, <u>Wallace</u> further discloses the set of biological

sequences comprises one or more of, nucleic acid sequences and amino acid

sequences (*Figure 4 shows for a new biological data search request, the user*

*enters a search description 71 in a search description text box 72, followed by*

*either a new set of FASTA formatted sequences 73 in a formatted sequence set*

*text box 74, a local file 75 in a local file text box 76, or an existing sequence set*

*77 in an existing sequence set text box 78*, [Column 7, Line 63 → Column 8, Line

2]).

Regarding **claim 98**, <u>Wallace</u> further discloses receiving the set of

biological sequences comprises receiving the set of biological sequences from a

user (*Figure 4 shows for a new biological data search request, the user enters a*

*search description 71 in a search description text box 72, followed by either a*

*new set of FASTA formatted sequences 73 in a formatted sequence set text box*

*74, a local file 75 in a local file text box 76, or an existing sequence set 77 in an*

*existing sequence set text box 78*, [Column 7, Line 63 → Column 8, Line 2]).


Regarding **claim 99**, <u>Algate</u> further discloses the query results further

comprise complementary deoxyribonucleic acid (eDNA) data, expressed

sequence tags, and pharmacology data (*Initial characterization of the cDNA*

*expression library was performed by randomly sequencing 24 primary*

*transformants and subjecting the resulting sequences to BLAST searches*

*against available databases. The determined cDNA sequences are provided in*

*SEQ ID NO: 443-480, with the results of the BLAST searches being provided in*

*Table 4*, [0998]), expressed sequence tags (*Comparison of the isolated*

*sequences with those in the public database revealed no significant homologies*

*to the sequences of SEQ ID NO: 151, 153 and 154. The sequences of SEQ ID*

*NO: 149, 152, 156, 157 and 158 were found to show some homology to*

*previously isolated expressed sequence tags (ESTs)*, [0973]).


Regarding **claim 100**, <u>Wallace</u> further discloses performing one or more

bioinformatics functions on the set of biological sequences or the query results

(*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary. The search summary is presented as a table 101 listing out in columns the search name 102, requested user 103, date 104, sequence set 105, databases 106, and deletion flag 107. The table 101 is necessary to display the individual results based on the specified database and requesting sequence, as each search can include multiple sequences and multiple databases. Individual search results can be deleted by pressing the "Delete Searches" button 108. Detailed search results can be obtained by selecting an appropriate search name 102*, [Column 8, Lines 35-45]).

Regarding **claim 101**, <u>Wallace</u> further discloses the one or more bioinformatics functions comprises one or more of sequence alignment, gene identification, protein identification structure prediction, motif comparison, and biological text analysis (*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary. The search summary is presented as a table 101 listing out in columns the search name 102, requested user 103, date 104, sequence set 105, databases 106, and deletion flag 107. The table 101 is necessary to display the individual results based on the specified database and requesting sequence, as each search can include multiple sequences and multiple databases. Individual search results can be deleted by pressing the "Delete Searches" button 108. Detailed search results can be obtained by selecting an appropriate search name 102*, [Column 8, Lines 35-45]).

Regarding **claim 102**, <u>Wallace</u> further discloses displaying an executive summary of the record of one of the set of biological sequences comprises formatting the requested record for output to the user (*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for displaying a search summary. The search summary is presented as a table 101 listing out in columns the search name 102, requested user 103, date 104, sequence set 105, databases 106, and deletion flag 107. The table 101 is necessary to display the individual results based on the specified database and requesting sequence, as each search can include multiple sequences and multiple databases. Individual search results can be deleted by pressing the "Delete Searches" button 108. Detailed search results can be obtained by selecting an appropriate search name 102*, [Column 8, Lines 35-45]).

Regarding **claim 103**, <u>Wallace</u> further discloses a system for managing a biological database (*Figure 1*), comprising:

a target database node, comprising a first memory and a first processor, wherein the first processor is configured to receive and store query results in the biological database, wherein the biological database comprises a set of biological sequences (*The relational database 33 stores tables and queues relating to search requests and results as transacted by the Blast Node 18*, [Column 4, Lines 65-67]. *A set of search query parameters specifying a plurality of sequence sets are received*, [Column 3, Lines 12-14]).

a functional node, comprising a third memory and a third processor,

wherein the third processor is configured to periodically query the plurality of

databases on the query database node with the set of biological sequences from

the target database node and send query results to the target database node

(*During each iteration (block 232), the Blast node 53 searches the search queue*

*43 (shown in FIG. 2) for those entries having a status equal to zero (block 233).*

*A status of zero indicates that no search results are present. If no entries are*

*found (block 234), the Blast node 53 sleeps for a pre-determined interval (block*

*235). In the described embodiment, an interval of 2,000 milliseconds is used,*

*although other suitable intervals could also be used*, [Column 11, Lines 4-12]);

and

a network switch node, comprising a fourth memory and a fourth

processor, wherein the fourth processor is configured to direct the receipt and

storage of query results in the biological database, the periodic download and

storage of the plurality of databases, and the periodic query of the plurality of

databases on the query database node (*Figures 1 and 11*).

Algate discloses the results comprise at least comprise at least

immunohistological data, *in situ* hybridization data, functional data, expression

data, and structural data ([0723] and [0809]).

It would have been obvious to an ordinary person skilled in the art at the

time of the invention was made to incorporate the teachings of Algate with the

teachings of Wallace for the purpose of utilizing polypeptides and polynucleotides

to produce pharmaceutical compositions, e.g., vaccines, and other compositions

for the diagnosis and treatment of lung cancer ([0002] of <u>Algate</u>).

Gibson discloses:

a query node, comprising a second memory and a second processor,

wherein the second processor is configured to periodically download and store a

plurality of databases from an external network (*Figure 1 shows the PRID system*

*10 includes client systems 16a, 16b, and 16c. Each client has applications and a*

*local mirror database 17a, 17b, and 17c, [0024]. Periodically, an update file is*

*created for each client with all relevant changes since the last modification of the*

*client database. When the clients systems 16(a-c) connect to the server 11, the*

*modification files associated with the client are transmitted to the client to be*

*used for updating each client's individual database, [0025]*);

It would have been obvious to an ordinary person skilled in the art at the

time of the invention was made to incorporate the teachings of <u>Gibson</u> with the

teachings of <u>Wallace</u>, as modified by <u>Algate</u>, for the purpose of creating update

drug data for addition to the original drug information, and a transmit mechanism

that transmits the update drug data to the remote device upon receiving a

request from a remote device for the update drug data ([Abstract] of <u>Gibson</u>).


Regarding **claim 104**, <u>Wallace</u> further discloses the set of biological

sequences comprises one or more of, nucleic acid sequences and amino acid

sequences (*Figure 4 shows for a new biological data search request, the user*

*enters a search description 71 in a search description text box 72, followed by*

*either a new set of FASTA formatted sequences 73 in a formatted sequence set*

*text box 74, a local file 75 in a local file text box 76, or an existing sequence set*

*77 in an existing sequence set text box 78,* [Column 7, Line 63 → Column 8, Line

2]).

Regarding **claim 105**, Wallace further discloses the functional node is

further configured to perform one or more bioinformatics functions on the set of

biological sequences or the query results and update the target database node

(*FIG. 6 is a screenshot 100 showing, by way of example, a Web page for*

*displaying a search summary. The search summary is presented as a table 101*

*listing out in columns the search name 102, requested user 103, date 104,*

*sequence set 105, databases 106, and deletion flag 107. The table 101 is*

*necessary to display the individual results based on the specified database and*

*requesting sequence, as each search can include multiple sequences and*

*multiple databases. Individual search results can be deleted by pressing the*

*"Delete Searches" button 108. Detailed search results can be obtained by*

*selecting an appropriate search name 102,* [Column 8, Lines 35-45]).

Regarding **claim 106**, Wallace further discloses the one or more

bioinformatics functions comprises one or more of sequence alignment, gene

identification, protein identification structure prediction, motif comparison, and

biological text analysis (*FIG. 6 is a screenshot 100 showing, by way of example,*

*a Web page for displaying a search summary. The search summary is presented*

*as a table 101 listing out in columns the search name 102, requested user 103,*

*date 104, sequence set 105, databases 106, and deletion flag 107. The table 101*

*is necessary to display the individual results based on the specified database*

*and requesting sequence, as each search can include multiple sequences and*

*multiple databases. Individual search results can be deleted by pressing the*

*"Delete Searches" button 108. Detailed search results can be obtained by*

*selecting an appropriate search name 102*, [Column 8, Lines 35-45]).

Regarding **claim 107**, <u>Wallace</u> further discloses the plurality of databases

comprises two or more of, National Center for Biotechnology Information (NCBI)

databases or other externally curated and maintained specialized databases

(*Figure 6*).

Regarding **claim 108**, <u>Wallace</u> further discloses the query node is further

configured to periodically download and store a plurality of databases from an

external network daily (*During each iteration (block 232), the Blast node 53*

*searches the search queue 43 (shown in FIG. 2) for those entries having a status*

*equal to zero (block 233). A status of zero indicates that no search results are*

*present. If no entries are found (block 234), the Blast node 53 sleeps for a pre-*

*determined interval (block 235). In the described embodiment, an interval of*

*2,000 milliseconds is used, although other suitable intervals could also be used,*

[Column 11, Lines 4-12]).

Regarding **claim 109**, Algate further discloses the query results further

comprise complementary deoxyribonucleic acid (eDNA) data, expressed

sequence tags, and pharmacology data (*Initial characterization of the cDNA*

*expression library was performed by randomly sequencing 24 primary*

*transformants and subjecting the resulting sequences to BLAST searches*

*against available databases. The determined cDNA sequences are provided in*

*SEQ ID NO: 443-480, with the results of the BLAST searches being provided in*

*Table 4*, [0998]), expressed sequence tags (*Comparison of the isolated*

*sequences with those in the public database revealed no significant homologies*

*to the sequences of SEQ ID NO: 151, 153 and 154. The sequences of SEQ ID*

*NO: 149, 152, 156, 157 and 158 were found to show some homology to*

*previously isolated expressed sequence tags (ESTs)*, [0973]).


Regarding **claim 110**, Wallace further discloses each of sequences in the

set of biological sequences is associated with a record comprising query results

from each of the plurality of databases (*Each biological data repository contains*

*sequence data stored into unstructured records which are each identified by a*

*unique identifier. The structured database query is executed against at least one*

*database engine. The database results are obtained from the selected biological*

*data repositories*, [Column 3, Lines 35-40]).

Regarding **claim 112**, <u>Wallace</u> further discloses the target database node

is further configured to format the requested record for output to the user (*FIG. 6*

*is a screenshot 100 showing, by way of example, a Web page for displaying a*

*search summary. The search summary is presented as a table 101 listing out in*

*columns the search name 102, requested user 103, date 104, sequence set 105,*

*databases 106, and deletion flag 107. The table 101 is necessary to display the*

*individual results based on the specified database and requesting sequence, as*

*each search can include multiple sequences and multiple databases. Individual*

*search results can be deleted by pressing the "Delete Searches" button 108.*

*Detailed search results can be obtained by selecting an appropriate search name*

*102*, [Column 8, Lines 35-45]).

## Conclusion

10.     These following prior arts is/are made of record and not relied upon are

considered pertinent to Applicant's disclosure:

<u>Bjornson</u> (*Pub. No. US 2002/0194173*) teaches method and apparatus for

high-performance sequence comparison.

The Examiner requests, in response to this Office action, support(s) must

be shown for language added to any original claims on amendment and any new

claims. That is, indicate support for newly added claim language by specifically

pointing to page(s) and line no(s) in the specification and/or drawing figure(s).

This will assist the Examiner in prosecuting the application.

When responding to this office action, Applicant is advised to clearly point out the patentable novelty which he or she thinks the claims present, in view of the state of the art disclosed by the references cited or the objections made. He or she must also show how the amendments avoid such references or objections See 37 CFR 1.111(c).

### *Contact Information*

11.     Any inquiry concerning this communication or earlier communications from the Examiner should be directed to Son T. Hoang whose telephone number is (571) 270-1752. The Examiner can normally be reached on Monday – Friday (7:00 AM – 4:00 PM).

If attempts to reach the Examiner by telephone are unsuccessful, the Examiner's supervisor, Neveen Abel-Jalil can be reached on (571) 272-4074. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service

Representative or access to the automated information system, call 800-786-

9199 (IN USA OR CANADA) or 571-272-1000.

/S. T. H./
Examiner, Art Unit 2165
November 30, 2009

/Neveen  Abel-Jalil/
Supervisory Patent Examiner, Art Unit 2165